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Review Article

Diversity and Function of Soil Microbiota in the Recovery of Degraded Areas: Ecological Bases and Biotechnological Applications

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Abstract

Soil constitutes one of the most complex and biodiverse ecosystems on the planet, harboring a vast community of microorganisms with a central role in maintaining biogeochemical processes and the sustainability of terrestrial ecosystems. This article reviews the diversity, structure, and ecological functions of the soil microbiota, with emphasis on its contribution to the recovery of degraded areas. The main microbial groups (bacteria, archaea, fungi, protists, and viruses) are discussed, highlighting their interactions, metabolic strategies, and role in nutrient cycling, soil structure formation, and promotion of plant growth. The influence of abiotic and biotic factors on the organization of microbial communities is also addressed, as well as the methodological advances that allow their characterization, including molecular and omics approaches. Additionally, the work explores the impacts of environmental degradation on the edaphic microbiota and the consequences for soil functionality, highlighting the loss of diversity and essential ecosystem services. In this context, microbiological strategies applied to ecological restoration are presented, such as inoculation of beneficial microorganisms, use of microbial consortia, soil translocation, and promotion of plant-microorganism interactions. Finally, the relevance of soil microbiology as a strategic tool for the recovery of ecological functionality is highlighted, especially in sensitive biomes such as the Caatinga, reinforcing the need to integrate the microbiota into environmental restoration projects.

Keywords: *Soil science, Metagenomics, Rhizosphere, Bioprospecting, Ecological succession*

1. Introduction

The term “soil” refers to the loose outer material of the Earth’s surface, a distinct layer above the underlying bedrock, and constitutes an essential natural resource for living organisms. It is a central component of the Earth and deserves special status due to its role in regulating the terrestrial environment, thereby influencing the sustainability of life on the planet, while also serving as a complex habitat [1]. Such complexity governs soil biodiversity, since it is estimated that soil contains about one-third of all living organisms and regulates the activity of organisms responsible for the functioning and evolution of ecosystems [2].

The concept that the physicochemical properties of the Earth are closely coupled with the activity of the living organisms it sustains was proposed in the early 1970s through the Gaia hypothesis [3]. According to this hypothesis, the Earth behaves as a superorganism with the intrinsic capacity to regulate its own climate and chemistry, thereby maintaining an environment favorable to life. In turn, soil possesses the intrinsic capacity to sustain terrestrial life and to provide a habitat for the existence and evolution of the organisms that inhabit it [4,5].

Based on this hypothesis, scientists launched the Global Soil Biodiversity Initiative with the aim of assessing soil life across all biomes of the planet, considering the essential ecosystem services provided by soils (such as plant biomass production, decomposition, and nutrient cycling), as well as identifying regions where soil quality is threatened by human activities. The ultimate goal is to support environmental policies aimed at sustainable land management [6-8].

2. Soil Structure and Complexity as a Microbial Habitat

From this understanding of soil as the foundation of ecosystem services, it becomes necessary to examine its constitution and internal organization. In terms of composition, vegetated soils generally present four main components: the inorganic mineral fraction (approximately 40% of the volume), organic matter (5%), air and water (50%), and soil biota, composed of macro- and microbiota (5%). This configuration demonstrates that soil is not an inert compartment, but rather a complex and dynamic habitat that harbors high microbial biodiversity. This habitat results from the continuous interaction between living organisms (microorganisms, plants, and animals) and the abiotic environment, whose structure is determined by factors such as parent material, climate, and vegetation, all modulated by abiotic variables [9-11].

In this context, the structural and physicochemical heterogeneity of soil leads to the formation of a wide diversity of microhabitats capable of sustaining extremely high biomass and a significant portion of the planet’s genetic diversity. It is estimated that Earth’s soils harbor approximately 2.6×10^{29} prokaryotic cells. A single gram of soil may contain kilometers of fungal hyphae, more than 10^9 bacterial and archaeal cells, and organisms belonging to tens of thousands of distinct species. In terms of biomass, soil biota may exceed 10 tons per hectare [12,13].

This diversity is favored by the intense spatial variability of the edaphic environment, in which well-aerated zones may be separated by only a few millimeters from regions with low oxygen availability. Similarly, surface layers tend to be enriched with decomposing organic matter and readily available nutrients, whereas the subsoil generally presents lower fertility. Within this environmental mosaic, the microenvironments associated with soil particle surfaces, where nutrients are concentrated, differ markedly from the soil solution, thereby conditioning the distribution, activity, and interactions of microorganisms [14,15].

Among the various soil microenvironments, the one directly influenced by plant roots, known as the rhizosphere, is particularly noteworthy. This region constitutes a zone of intense biological and chemical activity resulting from the continuous release of root exudates, such as sugars, amino acids, organic acids, and phenolic compounds. These substances alter the physicochemical conditions of the adjacent soil and provide energetic substrates for microorganisms, thereby recruiting specific microbial groups from the overall soil biodiversity. Consequently, the rhizosphere exhibits greater microbial abundance and activity compared with non-rhizospheric soil and exerts a strong selective effect on specific functional groups, favoring microorganisms associated with nutrient cycling, plant growth promotion, and pathogen suppression [16-18].

Thus, the rhizosphere is characterized by higher microbial abundance and activity than non-rhizospheric soil, a phenomenon known as the rhizosphere effect. As a result, the rhizosphere tends to harbor a functionally specialized microbial community that is often less taxonomically diverse, yet more efficient in carrying out ecological processes of interest, such as nutrient cycling, organic matter mineralization, and biological nitrogen fixation. In this way, the rhizosphere constitutes a fundamental link between soil microbial diversity and the functioning of terrestrial ecosystems [19].

Among the most relevant biological interactions occurring in the rhizosphere are mycorrhizal associations, established between plant roots and soil fungi, which represent one of the most widespread and ecologically important symbioses in terrestrial ecosystems. In these associations, mycorrhizal fungi partially or completely colonize root tissues, forming an extensive network of hyphae that extends beyond the root depletion zone, significantly increasing the volume of soil explored [20]. As a result, there is a marked increase in the absorption of poorly mobile nutrients, especially phosphorus, nitrogen, and micronutrients, as well as greater efficiency in water uptake [21,22].

In return, the plant supplies fungi with organic compounds derived from photosynthesis, establishing a mutualistic relationship based on the exchange of energetic and nutritional resources. Mycorrhizae also play a fundamental role in protecting roots against pathogens, enhancing plant tolerance to abiotic stresses such as drought and salinity, and improving soil structure through aggregate stabilization, thus constituting a key component of the rhizosphere and an essential link between soil microbial diversity, plant productivity, and ecosystem resilience [22,23].

Among the mycorrhizal associations established in the rhizosphere, two major types stand out: endomycorrhizae and ectomycorrhizae, which differ mainly in their root colonization patterns. In endomycorrhizae, also known as arbuscular mycorrhizae, fungi penetrate the cortical cells of roots, forming specialized structures such as arbuscules and vesicles that mediate intense nutrient exchange between fungus and plant [24]. This type of association is the most common and occurs in the majority of vascular plants, frequently involving fungi of the phylum Glomeromycota. In ectomycorrhizae, fungi do not invade plant cells but instead externally envelop the roots with a dense hyphal mantle and form an intercellular network known as the Hartig net, through which nutrient exchange occurs. This type of mycorrhiza is more common in woody plants, especially in temperate forests, involving fungi mainly from the phyla Basidiomycota and Ascomycota [25].

In addition to mycorrhizal associations, plants establish symbiotic interactions with soil bacteria, particularly the rhizobium–legume symbiosis responsible for biological nitrogen fixation, as well as less specific associations with plant growth-promoting rhizobacteria, which play a fundamental role in plant nutrition and adaptation to adverse edaphic environments. In the rhizobium–legume symbiosis, diazotrophic bacteria belonging to genera such as *Rhizobium* and *Bradyrhizobium* colonize plant roots and induce the formation of specialized root nodules [26]. Within these nodules, molecular nitrogen (N_2) is reduced to ammonia through the action of the enzyme nitrogenase, making nitrogen assimilable to the plant. In return, the plant supplies carbon-rich organic compounds and creates a physiologically regulated microenvironment with low oxygen levels, an essential condition for nitrogenase activity. This association represents one of the most efficient natural strategies for nitrogen supply in terrestrial ecosystems, being particularly relevant in poor or degraded soils where nitrogen availability is one of the main limiting factors for plant productivity [27,28].

Due to this remarkable microscopic diversity present in soils, soil microbiology has become established as a branch of microbiology dedicated to the study of the diversity, structure, metabolic functions, and interactions of edaphic microorganisms, as well as their direct influence on soil fertility, soil health, and ecosystem resilience. Historically, this scientific field began to take shape in the late nineteenth century, alongside the development of classical microbiology and agricultural chemistry. In this context, the pioneering works of Sergei and Martinus were fundamental in demonstrating that soil microorganisms play central roles in biogeochemical cycles. These discoveries, consolidated in the early twentieth century, broke with the perception of soil as merely a physical support for plants and instead recognized it as a biologically active and dynamic system. Decades later, advances in cultivation techniques, biochemistry, and, more recently, molecular and genomic approaches greatly expanded the understanding of soil microbial diversity and its interactions with plants, minerals, and organic matter, establishing soil microbiology as a central field for ecology, agriculture, and environmental biotechnology [29].

3. Diversity of Soil Microbiota

It is important to emphasize that the concept of microbial diversity refers to biological complexity and variability at different levels of organization. It encompasses genetic variability within taxa (biological diversity), as well as functional groups (functional diversity) within communities. At the ecosystem scale, microbial diversity is also expressed through the breadth of biogeochemical processes, the complexity of biological interactions, and the number of trophic levels involved [30-31].

Therefore, the assessment of soil microbial diversity requires integrative approaches that combine holistic methods capable of capturing the overall structure of communities with more specific analytical strategies directed toward structural or functional subsets. Such methodological integration is essential for a broader understanding of the organization, functioning, and resilience of soil ecosystems. It is estimated that a single gram of soil may harbor up to 10 billion (10^{10}) microorganisms. However, despite this abundance and complexity, less than 1% of the microorganism's observable by microscopy have actually been cultivated and characterized, highlighting that soil ecosystems remain largely unexplored from a microbiological perspective. The occurrence of such abundance and diversity is vital for soil functionality, since different organisms possess distinct physiological and ecological characteristics, thereby ensuring the occurrence of a wide range of soil processes under varying environmental conditions [32,33].

This diversity is directly related to a set of abiotic factors (atmosphere, temperature, water, pH, redox potential, nutritional sources, among others) and biotic factors (microbial genetics and interactions among microorganisms) that enable microbial development and the structuring of the living soil community. The interaction among these factors directly influences the ecology, activity, and population dynamics of soil microorganisms [34]. Considering abiotic factors, soil constitutes a highly heterogeneous and dynamic environment in which small variations in physicochemical conditions result in profound changes in the composition and activity of microbial communities. The soil atmosphere, especially oxygen availability, determines the predominant types of metabolism, favoring aerobic, microaerophilic, or anaerobic microorganisms depending on gas diffusion and local respiratory activity. Similarly, temperature acts as a regulatory factor for the rate of biochemical reactions, selecting microorganisms adapted to specific thermal ranges and directly influencing essential processes such as organic matter decomposition and nutrient transformation [35,36].

Water, in turn, plays a central role in soil microbiota, since it conditions solute diffusion, microbial motility, and oxygen availability, in addition to influencing pH. Soil pH also stands out as an important selective factor, affecting nutrient solubility, the toxicity of certain elements, and the structure of microbial communities, while directly influencing microbial enzymatic activity [37]. In addition to abiotic factors, biotic factors exert a decisive influence on the organization and functioning of soil microbial communities. Microbial genetics is one of the main biotic factors structuring soil communities, since it determines the set of metabolic, physiological, and ecological characteristics of microorganisms. The high genetic variability found in soils enables the coexistence of numerous microbial groups with different functional capacities, thereby broadening the spectrum of biological processes performed in this environment. This genetic diversity is directly related to niche specialization, metabolic efficiency, and the resilience of microbial communities to disturbances, contributing to the ecological stability of soil [38,39].

Interactions among microorganisms are determinant for soil ecological dynamics and may be classified as positive or negative according to their effects. Positive interactions include mutualistic symbioses and commensalism, in which at least one microorganism benefits without causing harm to the other, whereas negative interactions include antagonism, predation, and competition, characterized by detrimental effects on at least one of the participants. Thus, these biotic relationships contribute to the stability of microbial communities, influence soil ecological succession, and ensure the balance of biogeochemical processes essential to the functioning of terrestrial ecosystems. As a result of the integrated action of these environmental and biological factors, soil harbors a wide variety of microorganisms whose composition and abundance vary according to local conditions, characterizing a high level of biological diversity, particularly with regard to the taxonomic diversity of microbial communities. As previously mentioned, this diversity includes bacteria, archaea, fungi, protists, and viruses [40-42].

3.1 Bacteria and Archaea

In this context, among the various groups of microorganisms that compose soil biota, bacteria and archaea stand out as the most abundant, diverse, and functionally relevant organisms. These microorganisms belong to the group of prokaryotes and are traditionally distinguished from eukaryotes (fungi, algae, protozoa, plants, and animals) by structural and functional characteristics, such as the absence of a membrane-bound nucleus, the presence of 70S ribosomes, and the relatively simple organization of the cellular apparatus [43,44]. Despite this apparent simplicity, bacteria and archaea exhibit extraordinary phylogenetic and metabolic diversity, greatly surpassing that of eukaryotic organisms. In soil, these groups play central roles in major biogeochemical processes, including the decomposition of organic matter, nutrient cycling (carbon, nitrogen, sulfur, and phosphorus), and the transformation of mineral and organic compounds. Furthermore, their high capacity to adapt to contrasting microenvironments as a result of abiotic factors gives these microorganisms a strategic role in maintaining the functionality of edaphic ecosystems [45].

Studies on the composition of soil prokaryotic communities based on 16S rRNA gene sequence analyses reveal a clear predominance of certain bacterial phyla. Within the domain Bacteria, the phylum Pseudomonadota accounts for nearly half of the identified species. Other abundant bacterial phyla include Acidobacteriota, Bacteroidota, Actinomycetota, and Bacillota. In addition, a significant proportion of soil phylotypes remains unclassified, indicating the presence of bacterial lineages that are still poorly known or rare, which further contributes to the complexity of the soil microbiome [46-49]. The dominance of these bacterial phyla in soils can be attributed to ecological and physiological characteristics that make them especially adapted to this environment. First, they exhibit great metabolic plasticity, that is, the ability to use diverse sources of carbon and energy. This versatility enables them to participate intensively in organic matter decomposition and nutrient mineralization, processes essential for carbon cycling and humus formation. Moreover, these groups display high ecological dispersal capacity, allowing them to colonize and persist in soils under a wide range of environmental conditions [50].

This adaptability is expressed across different soil textures and abiotic factors, as well as under distinct nutrient levels and management practices. Such versatility is reflected in species-level diversity, with estimates suggesting that 1 g of soil may contain more than 10,000 bacterial species. Thus, even in the face of natural and anthropogenic environmental variations, these bacterial phyla remain present and active, ensuring the continuity of biological processes fundamental to soil dynamics and fertility [51]. In comparison, the diversity of archaea in soils appears to be lower, with relatively few sequences representing the main archaeal phyla, such as Euryarchaeota, Thaumarchaeota, and Crenarchaeota. The lower diversity of archaea reported in studies may result from methodological limitations and the comparatively limited research focus on this group, rather than from their actual scarcity in soils [52]. Therefore, it is possible that the true diversity of soil archaea is much greater, and that emerging techniques such as metagenomics, metatranscriptomics, and targeted cultivation approaches will reveal a broader diversity with more complex ecological functions [53].

3.2 Fungi

Fungi exhibit high biodiversity, the true magnitude of which remains the subject of intense scientific debate. Although approximately 155,000 species have been formally described, estimates based on molecular approaches and the fungus-to-plant ratio suggest that the actual number of fungal species may reach about 1.5 million [54]. This discrepancy largely results from the presence of cryptic species, the limited number of specialized taxonomists, and the complexity of fungal life cycles. Recent studies indicate that many species traditionally considered cosmopolitan actually comprise species complexes with restricted geographic distributions and greater ecological specificity [55].

Fungi, in turn, stand out as dominant components of microbial biomass and metabolic activity, especially within the organic horizons of soils. Unlike the previously mentioned groups, fungi belong to the domain Eukarya and are predominantly multicellular organisms whose cells possess a membrane-bound nucleus and a cell wall rich in chitin. Although their numerical diversity is lower than that of prokaryotes, fungi perform essential ecological roles in soils, acting decisively in the decomposition of organic matter, carbon and nutrient cycling, and the physical structuring of soil through the formation and stabilization of aggregates [56].

Fungal biomass in soils is highly variable both among and within terrestrial biomes, being influenced by factors such as litter composition, root density, and nutrient availability. The relative abundance of fungi tends to increase in acidic, nutrient-poor soils with high carbon-to-nitrogen ratios, conditions under which bacterial activity is relatively reduced.

However, recent evidence indicates that fungal distribution in soils is more strongly regulated by nitrogen and phosphorus availability than exclusively by pH. Based on global studies of soil fungal diversity, the most predominant phyla, in decreasing order of abundance, are Ascomycota, followed by Basidiomycota and then Mucoromycota, whereas Chytridiomycota generally occur in lower relative abundance, although they perform specific and ecologically relevant functions within soil ecosystems [57,58].

Among the main taxonomic groups of fungi found in soils, the phylum Ascomycota is particularly noteworthy, consisting predominantly of saprobic fungi that efficiently participate in decomposition and nutrient cycling. In addition, this phylum includes symbiotic species associated with plant roots, as well as pathogenic species capable of affecting plants and other soil components. Due to their high taxonomic and functional diversity, Ascomycota confer considerable ecological plasticity to soil fungal communities, thereby contributing to the stability, resilience, and functioning of terrestrial ecosystems [59,60].

The phylum Basidiomycota represents another highly relevant group, especially because of its role in the decomposition of recalcitrant compounds such as lignin and in the formation of ectomycorrhizal associations. These fungi play a fundamental role in forest ecosystems, where they regulate carbon dynamics and facilitate nutrient uptake by host plants. Furthermore, lignicolous saprophytic basidiomycetes are essential for the degradation of complex plant material, enabling the recycling of chemical elements in soils and contributing directly to soil fertility [61].

The phylum Mucoromycota, frequently cited in studies of soil fungal diversity, comprises fungi characterized by rapid growth and predominantly saprobic activity, being especially important during the early stages of organic matter decomposition. These fungi rapidly colonize plant residues rich in easily degradable compounds, contributing to the initial release of nutrients into the soil. Other phyla, although less abundant, also contribute significantly to the biological and functional diversity of soil fungi. Chytridiomycota occur mainly in moist environments and may act either as decomposers or parasites. Together, these groups demonstrate that soil fungal diversity extends beyond taxonomic richness, reflecting a broad range of functions essential for the sustainability and balance of terrestrial ecosystems [62]. The structure of soil fungal communities is also influenced by dispersal mechanisms. Although fungi can disperse through airborne spores, most spores are deposited close to the organism of origin, making long-distance dispersal relatively rare. Factors such as dispersal capacity, habitat adaptation, and host specificity determine the biogeographic patterns of soil fungi [63,64].

3.3 Protists

Protists constitute a diverse and functionally relevant group of eukaryotic microorganisms present in soils, playing fundamental roles in ecological dynamics and biogeochemical processes within this environment. This group mainly includes protozoa, microscopic algae, and fungus-like protists, such as myxomycetes and oomycetes, whose taxonomic and functional diversity remains underestimated compared with that of bacteria and fungi [65].

Although they represent a smaller fraction of soil microbial biomass, protists exert significant influence on the structure and functioning of microbial communities. These organisms act predominantly as consumers, occupying higher trophic levels within the microbial food web, especially through the predation of bacteria, archaea, and fungi. In this way, they regulate the population abundance of these microorganisms, influence microbial community composition, and indirectly modulate processes such as nutrient mineralization and carbon and nitrogen cycling. The predatory activity of protists in soil is closely associated with the concept of the microbial loop, in which bacterial biomass is recycled by microbial consumers, resulting in the release of inorganic nutrients that become available to plants and other microorganisms [66,67].

From a taxonomic perspective, the diversity of soil protists is extremely broad and heterogeneous, reflecting the polyphyletic nature of this group. Among the principal groups found in edaphic environments are amoeboid protozoa, flagellates, and ciliates, each exhibiting distinct ecological strategies. In addition to heterotrophic protozoa, soils also harbor microscopic algae and phototrophic protists, particularly in surface layers exposed to light. These organisms contribute to carbon fixation through photosynthesis, participate in soil surface stabilization, and act as primary sources of organic matter in newly formed or degraded environments. Their distribution and abundance are conditioned by both biotic and abiotic factors [66, 68].

3.4 Viruses

Viruses constitute another essential, yet historically underestimated, component of soil microbiota. Unlike other microbial groups, viruses are acellular entities composed basically of genetic material (DNA or RNA). Despite this structural simplicity and their obligatory dependence on host cells for replication, viruses are among the most abundant and diverse biological entities in soils, reaching between 10^8 and 10^{10} viral particles per gram of soil [69].

However, viral diversity remains underestimated, since metagenomic studies have revealed that most viral sequences recovered from soils show no similarity to previously described viruses, forming what is known as “viral dark matter.” This diversity reflects both the enormous variety of microbial hosts present in soils and the rapid evolutionary processes characteristic of viruses. Thus, viruses represent one of the largest reservoirs of genetic diversity in the biosphere. In addition to regulating microbial populations, viruses can modulate the metabolism of their hosts, influencing organic matter degradation and nutrient cycling, which reinforces their role as functional regulators of biogeochemical processes [70,71].

In edaphic environments, most known viruses correspond to bacteriophages, that is, viruses that infect bacteria, although viruses of archaea, fungi, protists, and plants are also present. These viruses play a central role in regulating microbial populations through infection and cell lysis, directly influencing microbial community structure. Viral lysis results in the release of carbon, nitrogen, phosphorus, and other nutrients contained within microbial biomass, making them available once again in the environment. This process, known as the viral shunt, represents an alternative pathway for nutrient recycling, diverting part of the organic matter flow away from classical trophic chains and intensifying biogeochemical cycling [72-74].

From an ecological perspective, soil viruses exert selective control over their hosts, often described by the “kill-the-winner” model, in which the most abundant microbial populations are preferentially infected and reduced through viral activity. This mechanism helps prevent the excessive dominance of particular groups, thereby promoting greater diversity and stability. Alternatively, many viruses exhibit lysogenic life cycles, in which the viral genome is integrated into the host genome and passively replicated during cell division [75].

The genetic diversity of soil viruses is extraordinary and remains largely unknown. Nevertheless, recent studies have demonstrated the predominance, in more than 50% of viral genomes, of the bacteriophage families Siphoviridae and Myoviridae. In contrast, mycoviruses (viruses that infect fungi) are less abundant and less diverse. Most viruses associated with eukaryotes possess RNA genomes and generally live as endosymbionts without causing evident symptoms. Their transmission occurs mainly vertically through spores or horizontally through hyphal contact, allowing their dissemination among fungi [76,77].

3.5 Studies in Brazilian Ecosystems

Given the high diversity of soil microorganisms, it becomes essential to understand how these communities are organized and function across different ecosystems, including the Brazilian phytogeographic domains. However, knowledge regarding microbial diversity in Brazilian natural areas remains relatively limited. As a consequence, many domains remain under-sampled, making it difficult to establish a comprehensive overview of microbial diversity and its functional roles within Brazilian ecosystems [78].

Among the most extensively studied environments, the Amazon stands out, where much of the research has focused on the effects of deforestation and land-use change on soil microbial communities. Evidence indicates that the conversion of forest areas into pastures or agricultural systems promotes microbial homogenization, with a reduction in β-diversity, reflecting the loss of environmental heterogeneity characteristic of natural ecosystems. This process is frequently associated with the physical disruption of soil structure, increased nutrient exposure, and the reorganization of ecological niches available to microorganisms [79].

The Caatinga, an exclusively Brazilian domain of seasonally dry tropical forests, remains poorly studied from a microbiological perspective despite its remarkable ecological uniqueness. Its soils, characterized by a semiarid climate, high seasonality, and intense environmental pressure, select for microorganisms adapted to water stress, high temperatures, and low nutrient availability. Available studies indicate the predominance of heterotrophic mesophilic bacteria, often spore-forming, as well as actinobacteria, suggesting the occurrence of adaptive strategies directed toward resistance, persistence, and survival under adverse environmental conditions [80,81].

4. Soil Microbiology in the Recovery of Degraded Areas

In this context, microorganisms play a leading role in providing essential ecosystem services that sustain the functionality, stability, and productivity of natural and agricultural ecosystems. These services correspond to the ecological functions and biotechnological resources supplied by soil microbiota and are fundamental for maintaining the physical, chemical, and biological processes that occur within soils. Among the principal ecosystem services provided by soil microorganisms are the cycling of organic matter and nutrients, especially nitrogen, processes that ensure residue decomposition, the release of essential nutrients, humus formation, and the maintenance of soil fertility and structure. In addition, soil microbiota participate in pedogenesis and support regulatory and biotechnological services, such as the bioremediation of contaminants and the biological control of pathogenic organisms, thereby contributing to soil resilience and to the stability of natural and agricultural systems. Soil microorganisms also sustain food webs and plant productivity, being strategically important for ecosystem functioning through the integration of nutrient cycling, environmental regulation, and agricultural production [82-84].

In this regard, understanding the functional role of soil microorganisms becomes especially relevant in the context of degraded land recovery, since these organisms are directly involved in restoring soil fertility, structure, and biogeochemical processes. The restructuring of microbial communities constitutes a fundamental step for reestablishing nutrient cycling, biological activity, and plant productivity, thereby acting as the basis for ecological succession and the recovery of ecosystem functionality. Given the high diversity and complexity of soil microbiota, understanding their diversity and functional roles requires the application of appropriate analytical techniques. In general, these approaches can be grouped into cultivation-dependent methods, biochemical and physiological methods, and molecular and omics-based methods, which, in a complementary manner, enable the investigation of the structure and functioning of edaphic microbial communities [85,86].

Historically, the study of soil microorganisms was based on cultivation-dependent methods such as colony-forming unit counts, most probable number estimates, and the isolation of strains in artificial media. These approaches enable the quantification of viable microorganisms and the performance of detailed physiological, biochemical, and taxonomic studies. However, such methods provide only a partial view of microbial communities, since they favor organisms adapted to laboratory conditions and underestimate the uncultivable fraction, which represents the majority of soil diversity. In general terms, only about <0.1% of soil microorganisms can be cultivated using traditional methods [87].

Consequently, other methods have been widely employed, particularly biochemical and physiological approaches that evaluate metabolic activity and the overall functioning of microbial communities. Among these approaches are measurements of soil respiration, carbon and nutrient mineralization, enzymatic activity, and lipid biomarker analyses (FAME and PLFA). These methods provide integrated information regarding microbial biomass and community metabolism, allowing inferences about the functional role of microorganisms in biogeochemical cycles, although they do not directly permit taxonomic identification of the organisms involved. With the advancement of molecular biology, techniques based on nucleic acid analysis revolutionized soil microbiology by enabling access to the uncultivable fraction of microbial communities. The direct extraction of genetic material from soil forms the basis of these approaches, making it possible to investigate both the taxonomic composition and the functional potential of microorganisms. Methods such as PCR, fingerprinting, hybridization, and microarrays expanded the capacity to compare microbial communities across different environments and edaphic conditions. Thus, the integrated use of these methods forms the basis for a consistent analysis of soil microbiota and is essential for ecological studies, including degraded land restoration [88,89].

Soil degradation resulting from anthropogenic activities such as deforestation, mining, intensive agriculture, excessive use of agrochemicals, and industrial pollution profoundly compromises microbial functionality. These disturbances alter the physical and chemical structure of soils, reduce organic matter content, and promote the simplification of microbial communities, leading to the loss of essential ecosystem functions. In this scenario, the recovery of degraded areas represents one of the major contemporary environmental and socioeconomic challenges, especially in regions subjected to intense anthropogenic pressure, such as the Caatinga [90].

In this context, soil microbiology assumes strategic importance in the restoration of degraded areas, since microorganisms are the principal agents responsible for the processes described throughout this text. When these environments become degraded, there is generally a reduction in microbial diversity and activity, compromising soil resilience and recovery. Therefore, the restoration of degraded areas must extend beyond the reestablishment of vegetation cover to include the restoration of soil ecological functions, in which microbiota play a strategic role. From this perspective, integrative tools such as the recovery wheel proposed by the Society for Ecological Restoration allow restoration progress to be assessed systematically by considering attributes related to biological composition, ecological functions, and ecosystem conditions, all of which involve central roles for soil microorganisms [91,92].

The planning of restoration projects requires the establishment of realistic goals, well-founded decisions regarding interventions, and the use of indicators capable of monitoring progress over time. Unfortunately, despite the global expansion of restoration initiatives and scientific advances in the field, many projects still fail to achieve their objectives because insufficient importance is attributed to soil microbiota. Therefore, the systematic inclusion of soil microbiota from the beginning of restoration projects, together with flora and fauna assessments, is essential for more accurately defining the trajectory and objectives of restored ecosystems [93].

Ecological restoration planning must consider the severity of degradation as the basis for defining goals and the level of intervention required. In this context, microbiota play a central role, since their absence or alteration may compromise the establishment of plant species, especially those dependent on mycorrhizal fungi. Alterations in native microbiota may also result from colonization by exotic species or from land use practices distinct from the original environmental condition. The prior identification of these barriers increases restoration success by enabling the strategic use of plant–soil interactions, such as inoculation with late-successional microbiota, thereby favoring plant diversity. Another important aspect is the definition of reference sites, since these areas serve as models for the desired conditions to be achieved. The soil and vegetation characteristics of these locations directly influence the composition and functioning of microbiota, meaning that there is no universally “ideal” soil microbiota. Desirable microbial communities should therefore be defined based on reference sites and functional criteria. Considering that microbiota exhibit high spatial variability, even within the same area, sampling designs must account for this heterogeneity through strategies such as stratified or systematic sampling. In this context, specific microorganisms, such as rhizobacteria and mycorrhizal fungi, may play relevant roles in ecosystem recovery [94,95].

Although the inclusion of soil microbiota can increase restoration success, this strategy involves financial costs and risks that require case-by-case cost–benefit analyses. There is no single approach applicable to all ecosystems, since soil microbiota are highly variable and rarely constitute the sole limiting factor in restoration processes. Therefore, decisions regarding investment in this component must consider project objectives and the degree of degradation of the soil’s physical, chemical, and biological properties. When degradation primarily affects vegetation while soils retain characteristics close to natural conditions, the simple restoration of vegetation cover may be sufficient to promote gradual microbiota recovery, often with a high probability of success. In contrast, under scenarios of severe degradation, where profound alterations occur, as is frequently observed in areas subjected to intensive agriculture, persistent abiotic legacies are formed that limit spontaneous microbial recolonization, making targeted interventions necessary. In this context, the integration of physicochemical and biological soil assessments is fundamental for identifying limiting factors and supporting decision-making processes [96,97].

Accordingly, the incorporation of experiments focused on microbiota within degraded environments, planned from the outset, makes it possible to overcome the limitations of purely observational studies and strengthen the identification of cause-and-effect relationships. Such experiments, involving replication, control, and randomization, allow the direct evaluation of how different interventions influence microbiota and their functions. Longitudinal studies, which monitor the same locations over time through repeated measurements, provide more robust evidence but require long-term monitoring. When it is not possible to wait for experimental results, methods capable of identifying causal relationships in observational data, such as causal modeling, may support decision-making by enabling the testing of complex hypotheses and guiding more efficient restoration planning [98].

In terms of mechanisms of action, soil microorganisms play a central role in soils affected by salinization, sodification, aridity, loss of organic matter, nutrient depletion, and contamination by heavy metals and toxic organic compounds. In saline and sodic soils, characterized by excess sodium (Na^+) adsorbed onto clay particles, plant growth-promoting bacteria have proven fundamental in soil recovery and quality improvement processes. These microorganisms contribute to reductions in pH, electrical conductivity, and exchangeable sodium concentration through the release of organic acids, ion exchange, or salt complexation, thereby mitigating the deleterious effects of sodicity on soil structure. In addition, many of these bacteria produce extracellular polymeric substances (EPS), which act as cementing agents that promote soil particle aggregation and reduce sodium-induced clay dispersion. These biological processes result in significant improvements in soil physical structure, including increased porosity, water infiltration, and aeration, all of which are essential for root development and microbial activity [99,100].

In degraded areas affected by water deficit, erosive processes, and low vegetation cover, soil microbiota act directly in increasing aggregate stability, moisture retention, and soil surface protection. In this context, arbuscular mycorrhizal fungi are particularly important, as they promote the formation of stable macroaggregates through the production of glomalin, a hydrophobic glycoprotein that functions as a cementing agent. The action of these fungi improves soil porosity, increases water infiltration and retention, and favors organic carbon sequestration. Complementarily, several cyanobacteria that form biological soil crusts play essential roles in surface stabilization in arid and semiarid environments through EPS production. By binding mineral particles together, they reduce water and wind erosion, increase moisture retention, and favor the formation of more stable microenvironments for plant establishment [101].

Regarding the availability and cycling of nutrients essential for plants, nitrogen-fixing microorganisms such as *Azotobacter* spp. and symbiotic species of the genus *Rhizobium* are fundamental for incorporating atmospheric nitrogen (N_2) into the soil–plant system, thereby reducing nutrient limitation in degraded areas. At the same time, phosphate-solubilizing bacteria release phosphorus from insoluble forms through the production of organic acids and phosphatase enzymes, while other microorganisms contribute to the solubilization of potassium present in primary and secondary soil minerals. Beyond macronutrients, micronutrient-mobilizing microorganisms produce siderophores capable of chelating iron (Fe) and facilitating its uptake by plants, in addition to enhancing the availability of zinc (Zn) and other trace elements [102,103].

When associated with organic amendments, these microorganisms increase enzymatic activity, organic matter decomposition, and carbon stocks, thereby improving soil fertility. These processes enhance nutrient-use efficiency, reduce dependence on mineral inputs, and increase the resilience of restored ecosystems. In areas contaminated by heavy metals, pesticides, and hydrocarbons, soil microorganisms exhibit high bioremediation potential. These microscopic organisms perform biosorption and bioaccumulation of heavy metals and promote their immobilization through precipitation and complexation mechanisms. Simultaneously, microorganisms capable of degrading organic compounds possess efficient enzymatic systems that transform pesticides and hydrocarbons into less toxic metabolites, thereby accelerating their degradation in edaphic environments. The use of microbial consortia further enhances bioremediation processes by broadening the diversity of available biochemical pathways and increasing contaminant transformation efficiency [104].

In this context, different restoration interventions that act directly on soil microbiota have been proposed as strategic tools for enhancing the recovery of degraded ecosystems. Among these approaches, the most established is whole-soil translocation, which consists of transferring soil from reference ecosystems to degraded areas, thereby simultaneously reintroducing microbial communities, seed banks, and organic matter. This strategy can direct both plant and microbial succession and generate long-term residual effects, although it presents limitations related to cost, logistics, and impacts on donor ecosystems. Alternatively, targeted microbial inoculations through isolated microbial cultures, suspensions, or selected consortia have also been employed. These techniques enable the introduction of microorganisms with specific functions while requiring smaller amounts of soil and reducing impacts on reference areas. However, their success strongly depends on compatibility among the inoculum, the host plant, and the physicochemical conditions of the soil. Seed enhancement using microbial additives represents another promising strategy, involving techniques such as coating, bioencapsulation, conditioning, and the use of extruded granules containing beneficial microbiota. These approaches enable the precise delivery of microorganisms directly into the germination zone, favoring early plant establishment and the formation of symbiotic interactions from the initial stages of development, making them particularly suitable for large-scale restoration projects [105-107].

Furthermore, targeted microbiota management may be fundamental in environments where the absence of particular microorganisms limits plant establishment. In such cases, microbial consortia tend to be more effective than isolated strains because they exhibit greater functional resilience. Nevertheless, the selection, cultivation, and maintenance of these communities represent important technical challenges. Finally, strategies based on promoting positive soil legacies through the use of plants capable of favorably shaping microbiota have demonstrated potential to increase plant fitness and tolerance to environmental stress. These microbial legacies may benefit subsequent plant generations, thereby contributing to the stability and resilience of restored ecosystems, particularly under climate change scenarios [108].

At the regional scale, the Caatinga is characterized by semiarid climatic conditions marked by irregular rainfall, high temperatures, and the predominance of shallow, stony soils poor in organic matter. These natural factors, combined with historical anthropogenic pressures, intensify degradation processes, promoting soil compaction, erosion, localized salinization, and the loss of biological fertility. In this scenario, soil microbiota assume a fundamental role in degraded land recovery and in combating desertification processes. Studies in the Caatinga indicate that soil degradation reduces microbial biomass, diversity, and activity, compromising nutrient cycling and organic matter mineralization, whereas conserved or regenerating areas exhibit more diverse microbial communities adapted to water stress [109,110].

In this context, recent studies indicate that arbuscular mycorrhizal fungi and rhizobia associated with native legumes play central roles in Caatinga soil recovery by enhancing water and nutrient uptake, promoting soil aggregation, and favoring biological nitrogen fixation. In addition, cyanobacteria protect soils against erosion and contribute to carbon and nitrogen incorporation, being especially important in severely degraded areas. Thus, restoration strategies should integrate the recovery of both vegetation and soil microbiota, recognizing microbiota as key elements for the functionality, resilience, and sustainability of ecosystems [111].

5. Conclusion

In conclusion, soil microbiota constitute an essential component for maintaining the functionality of terrestrial ecosystems, playing a central role in nutrient cycling, soil structuring, and the promotion of plant productivity. Environmental degradation significantly compromises these communities, reducing their diversity and affecting fundamental ecosystem services, which reinforces the need to incorporate the microbiological dimension into restoration processes. In this context, strategies based on the use of microorganisms, such as targeted inoculations, microbial consortia, and the management of plant–soil interactions, present great potential to accelerate the recovery of degraded areas. Thus, integrating soil microbiota into practical ecological restoration approaches not only increases the efficiency of interventions but also contributes to the long-term sustainability and resilience of ecosystems.

Conflict of Interest

The authors declare no conflict of interest.

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